

Data Sheet

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pYSG-IBA23

Cat. No.: 5-4623-00 Lot No.: 4623-	Version: 2.2 Revision Date: 04.03.2020
Description	 StarGate[®] Acceptor Vector designed for high-level expression in yeast containing the following elements: Copper inducible promoter (CUP1) for controlled high-level expression URA3 auxotrophy marker for selection after transformation (do not use URA3 for selection during expression) LEU2d auxotrophy marker for selection to increase plasmid copy number for expression (do not use LEU2d for selection after transformation) 2µ ori for episomal replication in yeast The expressed recombinant protein will be localized in the cytoplasm.
Yeast Expression	Cultivate transformed yeast cells under LEU2d selection until OD600 reaches 0.8 – 1.2 absorbance units. Induce protein expression by addition of copper sulphate to a final concentration of 0.5 mM.
Affinity tag	 The recombinant protein will contain two affinity tags: Strep-Tactin affinity tag (Strep-tagII) for the purification of recombinant protein via Strep-Tactin resins. The Strep-tagII is fused to the C-terminus of the recombinant protein. GST-tag (Glutathione-S-Transferase) for the purification of recombinant protein. The affinity tag is fused to the N-terminus of the recombinant protein. After purification the GST may be removed by digesting with PreScission™ Protease.
Resistance	Ampicillin
Form	5 μg, dissolved in 20 μl TE buffer, pH 8,0: 10 mM Tris-HCl, 1 mM EDTA
Concentration	250 ng/μl
Stability	12 months after shipping
Storage	recommended: 2-8 °C for frequent usage, -20 °C for long-term storage
Shipping	room temperature
Hazards	Product is not classified as hazardous according to (EC) No 1272/2008 [CLP]. A Material Safety Data Sheet is provided.

Note: The sequences have been compiled from information in the sequence database, published literature, and other sources, together with partial sequences obtained by IBA, however, the vectors have not been completely sequenced. PreScission[™] Protease is a trademark of GE HEALTHCARE

For research use only

Important licensing information

This product is based on StarGate, Strep-tag and GST-tag technologies covered by intellectual property (IP) rights and on completion of the sale IBA grants respective Limited Use Label Licenses to purchaser. IP rights and Limited Use Label Licenses for said technology are further described and identified at http://www.ibalifesciences.com/patents.html or upon inquiry at info@iba-lifesciences.com or at IBA GmbH, Rudolf-Wissell-Str. 28, 37079 Goettingen, Germany. By use of this product the purchaser accepts the terms and conditions of all applicable Limited Use Label Licenses.

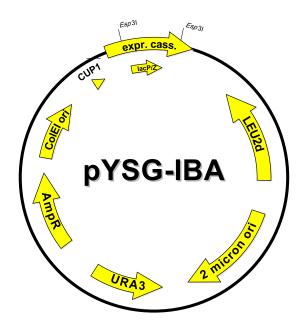
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Expression cassette of pYSG-IBA23

	GTI	'AG'I	GCI	AT A	ATCF	\TA1	rag <i>i</i>	AAGI	CA1	rcga	AAI	FAGA	ATAI	TAF	AGAF	AAA	ACAA	AACI	GTF	ACAF	ATCF	ATC	CATC	CACA	ATC	AATO	CATC	CACA	ΑI
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A	112 \TA1	113 TT <i>P</i>	114 AAA: N	115 IGGI G	116 FGAJ	117 TCAJ	- 118 FGT <i>I</i>	119 AACC	120 CA1	121 TCC1 P	122 TGAC	123 CTTC	124 CATC M	125 GTT(G	126 GTAI ST Y	127 IGAC	128	129 FCT1 L	130 TGAT	131 FGT1 V	132 IGT1 V	133 FTT <i>P</i>	134 ATAC Y	135 CATC M	136 GGA(D	137 137 CCC <i>I</i>	138 AATG M	139 GTGC C	20
: A	112 TAT Y 142	113 TT <i>F</i> L 143	114 AAA: N 144	115 IGGJ G 145	116 [GA] D 146	117 TCAT H 147	118 TGT <i>I</i> V 148	119 AACC T 149	120 CAT H 150	121 TCC1 P 151	122 TGAC D 152	123 CTTC F 153	124 CATC M 154	125 GTTC G L 155	126 GTA1 ST Y 156	127 CGAC D 157	128 CGC A 158	129 FCTT L 159	130 TGAT D 160	131 TGTT V 161	132 IGT1 V 162	133 FTT <i>P</i>	134 ATAC Y 164	135 CATC M 165	136 GGA(D 166	137 137 CCC <i>I</i> P 167	138 AAT G M 168	139 TGC C 169	20
: A	112 TAT Y 142	113 TT <i>F</i> L 143	114 AAA: N 144	115 IGGJ G 145	116 [GA] D 146	117 TCAT H 147	118 TGT <i>I</i> V 148 TTGT	119 AACC T 149	120 CAI H 150	121 FCC3 P 151	122 TGAC D 152	123 CTTC F 153	124 CATC M 154	125 GTTC L 155 AGCT	126 GTA1 ST Y 156	127 TGAC D 157	128 CGC: A 158	129 FCTT L 159	130 [GA] D 160	131 FGT1 V 161 FAAC	132 IGT1 V 162	133 FTT <i>P</i> L 163	134 ATAC Y 164 GAAP	135 CATC M 165	136 GGA(D 166 CAG(137 CCC <i>I</i> P 167 CAAC	138 AAT G M 168	139 TGC C 169	20
A	112 TAT Y 142 TGCC	113 TTT <i>F</i> 143 GTTC	114 AAA: N 144 CCC2	115 IGGJ G 145 AAAA K	116 ГGАЛ D 146 АТТ <i>Р</i> L	117 TCAJ H 147 AGTJ	118 FGT <i>I</i> V 148 FTGT	119 AACC T 149 FTTT	120 ССАЛ Н 150 ГАА <i>Р</i> К	121 FCC3 P 151 AAAA K	122 TGAC D 152 ACGI	123 CTTC F 153 FATT	124 CATC M 154 FGAA	125 GTTC G L 155 AGCJ A G A	126 GTAI ST 156 CATC ST	127 IGAC D 157	128 CGC A 158 ACA2	129 FCT1 159 AAT1	130 GAT 160	131 FGT1 V 161 FAAC	132 IGTJ 162 GTAC	133 TTTA L 163 CTTG L	134 ATAC Y 164 GAA <i>P</i>	135 CATC M 165 ATCC	136 GGA(D 166 CAG(S	137 137 CCC <i>P</i> 167 CAAC	138 AATG M 168 GTA1	139 GTGC C 169 CAT <i>I</i>	
A	112 TAT Y 142	113 TTT <i>F</i> 143 GTTC	114 AAA: N 144	IIS IGGJ G I45 AAAJ K	116 ГGАЛ 146 АТТ <i>Р</i>	117 TCAT H 147	118 FGT <i>I</i> V 148 FTGT	119 AACC T 149	120 CAI H 150	121 FCC3 P 151	122 TGAC D 152 ACGI	123 CTTC F 153	124 CATC M 154 FGAA	125 GTTC L 155 AGCT	126 GTAI ST Y 156 CATC	127 TGAC D 157	128 CGC: A 158	129 FCTT L 159	130 [GA] D 160	131 FGT1 V 161 FAAC	132 IGT1 V 162	133 FTT <i>P</i> L 163	134 ATAC Y 164 GAAP	135 CATC M 165	136 GGA(D 166 CAG(137 137 CCC <i>P</i> 167 CAAC	138 AAT G M 168	139 TGC C 169	
: A	112 112 Y 142 GCC A 172	113 TTT <i>P</i> L 143 TTTC F 173	114 N N 144 CCCC P 174	115 I G G J I 45 AAAA K 175	116 FGA1 D 146 ATT <i>P</i> L 176	117 ICAJ H 147 AGTJ V V 177	118 CGT <i>P</i> V 148 CTG7 C 178	119 AACCC T 149 F F 179	120 CCAI H 150 K K 180	121 PCCJ 151 XAAA K 181	122 CGAC D 152 ACGI R 182	123 CTTC F 153 FATT 183	124 CATC M 154 FGA <i>I</i> E 184	125 GTTC G 155 AGCJ A A 185	126 GTAI ST 156 CATC CATC I 186	127 CGAC D 157 CCC <i>2</i> P 187	128 CGCC A 158 ACAA 188	129 FCTT L 159 AATT 189	130 	131 FGTT V 161 FAAC K	132 IGTJ V 162 Y 192	133 TTTA L 163 CTTG L	134 ATAC Y 164 <i>K</i> 194	135 CATC M 165 ATCC S 195	136 GGA(D 166 CAG(S 196	137 137 P 167 167 K K 197	138 AATC M 168 168 Y 198	139 GTGC C 169 CAT <i>P</i> 199	
1 1	112 112 Y 142 GCC A 172	113 TTT <i>P</i> L 143 TTTC F 173	114 N N 144 CCCC P 174	115 FGGJ G 145 AAAA K K 175	116 FGA1 D 146 ATT <i>P</i> L 176	117 ICAJ H 147 AGTJ V V 177	118 CGT <i>P</i> V 148 CTG7 C 178	119 AAACC 149 F 179 CACC	120 CCAI H 150 K K 180	121 PCCJ 151 XAAA K 181	122 CGAC D 152 ACGI R 182	123 CTTC F 153 FATT 183	124 CATC M 154 FGA <i>I</i> E 184	125 GTTC G 155 AGCJ A A 185	126 GTAI ST 156 CATC CATC I 186	127 CGAC D 157 CCC <i>F</i> 187	128 CGCC A 158 ACAA 188	129 FCTT L 159 AATT 189	130 	131 FGTT V 161 FAAC K	132 IGTJ V 162 Y 192	133 FTT <i>P</i> L 163 CTTC L 193	134 ATAC Y 164 GAA <i>P</i> K 194	135 CATC M 165 ATCC S 195	136 GGA(D 166 CAG(S 196	137 137 P 167 167 K K 197	138 AATC M 168 168 Y 198	139 GTGC C 169 CAT <i>P</i> 199	A (
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1 1 3 6	112 Y 142 GGCC A A CGCC P P	113 TTT <i>P</i> L 143 TTC TTC TTC L L	N N 144 N 144 CCCC <i>L</i> P 174 GCA0 Q 204	115 IGGJ G 145 AAAAA K 175 GGGGC G	116 FGA1 D 146 ATT <i>P</i> 176 CTGC W 206	117 ICA1 H 147 AGT1 V V GCA <i>I</i>	118 CGT <i>I</i> V 148 CTGT 178 AGCCO A	119 AAACC T 149 F T77 179 CACC G G T T 209	120 CCAT H 150 CAA <i>F</i> 180 GTTT ST F 210	121 ГССЛ Р 151 К К 181 СССЛ 151	122 CGAC D 152 ACGI 182 CGGI	123 CTTC F 153 FATT 183 CGGC G Q 213	M T54 FGAA 184 CGAC	125 GTTC G 155 AGC1 185 CCA1	126 GTAI ST 156 CATC ST 186 CCCI	127 CGAC D 157 CCC <i>I</i> 187 CCC <i>I</i>		129 ICTI 159 AATI 189 AATC	TGA1 D 160 CGA1 190 GTCC S TCC	131 V 161 161 191 CGG <i>J</i> G	132 IGTJ V 162 GTAC Y 192 AGGJ G	L 133 L 163 CTTC L 193 CGGC	Y 134 Y 164 GAAA I94 CGGI	M 135 CATC M 165 ATCC S CGGC CCS G G	I 136 GGA(D 166 CAG(S 196 SAG() S		M M 168 GTA1 198 GGA <i>P</i>	139 GTGC C 169 CATA I 199 AGT1 V	A() :
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1 1 1 1 1 1 1	112 ATA1 Y 142 GGCC A 172 GCC1 P 202 CCAC	L L L 143 GTTC F TTTC L 203	N N 144 P 174 Q Q Q Q Q Q 174	115 G G 145 AAAAA K K 175 GGGC G 205	116 CGAT 146 ATTT 176 CTGC CTGC	н 117 ССАЛ 147 147 4GTT 177 GCA <i>H</i> 207	- 118 118 V V 148 CTGJ C T 178 AGCC A 208	119 AAACC T 149 F T77 179 CACC G G T T 209	H TI20 CCAT 150 CAAAA TI30 CAAAA TI30 ST TI30 ST 210	P T T T T T T T T T T T T T T T T T T T	122 CGAC D 152 ACGI 182 CGGI G G 212	123 CTTC F 153 FATT 183 G G G CGGC C 1 213 ite -	124 124 CATC M 154 E E 184 CGAC D 214	125 GTTC G 155 AGC1 185 CCA1	TI26 GTAI ST Y I I CATCC ST I I 186 CCCI 216	D 127 CGAC D 157 CCC <i>F</i> 187 187 217		129 CCTT L 159 AATT 189 AATT 219 <i>M</i> <i>M</i> <i>M</i> <i>Z</i> 19 <i>Z</i> 19 <i>Z</i> 19	TIGO TGAT D TIGO TGAT 190 STCC S S 220	V V IGTT IGT IGT IGT IGT IGT IGT IGGGA	132 V V 162 Y 162 Y 192 AGG 1 222	L 163 CTTTC L 163 CTTTC L 193 CTTCG G G G 223	Y Y I G G Z Z Z C A C C C C C C C C C C C C C C C	135 CATC M 165 ATCC S 195 CGGC CCS G CCS CCCC CCCC	D D 166 CAGO S 196 SAGO S 226	P 137 167 167 CCAAC K 197 197	138 AATC M 168 GTA1 198 GGA2 E 228	139 GTGC C 169 CAT <i>I</i> 199 AGTT V 229	
	112 ATA1 Y 142 GGCC A 172 GCC1 P 202 CCAC	113 "TT <i>P</i> L 143 "TTC F 173 "TTC L 203 GGGC	N N 144 P 174 Q Q Q Q Q Q 174	G G G G G G G G G G G G G G G G G G G	116 CGAT 146 ATTT 176 CTGC CTGC	н 117 ССАЛ 147 147 4GTT 177 GCA <i>H</i> 207	- 118 118 V V 148 CTGJ C T 178 AGCC A 208	119 AAACC T 149 F T77 179 CACC G G T T 209	120 CCA1 H 150 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 CAA7 CAA7 CAA7 CAA7 CAA7 CAA7 CAA	P 151 P 151 K K 181 CGG ¹ 211 gratic acP/	122 CGAC D 152 ACGI 182 CGGI 182 CGGI 212 CGGI 212 CGGI 212 CGGI 212 CGGI	123 CTTC F 153 F 153 FATT 183 CGGC G G 213 ite - 3 bp	124 124 CATC M 154 E E 184 CGAC D 214	125 GTTC G 155 AGC1 185 CCA1	TI26 GTAI ST Y I I CATCC ST I I 186 CCCI 216	D 127 CGAC D 157 CCC <i>F</i> 187 187 217		129 CCTT L 159 AATT 189 AATT 219 <i>M</i> <i>M</i> <i>M</i> <i>Z</i> 19 <i>Z</i> 19 <i>Z</i> 19	TIGO TGAT D TIGO TGAT 190 STCC S S 220	V V IGTT IGT IGT IGT IGT IGT IGT IGGGA	132 V 162 STAC Y 192 G G CGGZ	L 133 L 163 CTTC L 193 CCTTC G CTTC CCTTC 223	134 ATAC Y 164 G G G G CGGI PC CGGI 224	135 CATC M 165 ATCC S 195 CGGC CS G 225	D D 166 CAGO S 196 SAGO S 226	P 167 167 CCAAC K 197 227 FTCC	138 AATC M 168 GTA1 198 GGA2 E 228	139 GTGC C 169 CAT <i>I</i> 199 AGTT V 229	
1 AT 1 5 G	112 Y 142 Y 142 CGCC A 172 GCCT P 202 CCAC	113 "TT <i>I</i> L 143 GTTC F 173 "TTC L 203 GGGG	N N 144 P 174 Q Q Q Q Q Q 174	G G G G G G G G G G G G G G G G G G G	116 CGAT 146 ATTT 176 CTGC CTGC	н 117 117 117 117 1177 1177 GCA <i>H</i> 207	- 118 118 V V 148 CTGJ C T 178 AGCC A 208	119 AAACC T 149 F T77 179 CACC G G T T 209	120 CCA1 H 150 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 T30 CAA7 CAA7 T30 CAA7 CAA7 CAA7 CAA7 CAA7 CAA7 CAA7 CAA	P 151 P 151 K K 181 CGG ¹ 211 gratic acP/	122 CGAC D 152 ACGI 182 CGGI G G 212 212 DDN S	123 CTTC F 153 F 153 FATT 183 CGGC G G 213 ite - 3 bp	124 124 CATC M 154 E E 184 CGAC D 214	125 GTTC G 155 AGC1 185 CCA1	TI26 GTAI ST Y I I CATC CST I I I 186 CCCI I 216	D 127 CGAC D 157 CCC <i>F</i> 187 187 217		129 CCTT L 159 AATT 189 AATT 219 <i>M</i> <i>M</i> <i>M</i> <i>Z</i> 19 <i>Z</i> 19 <i>Z</i> 19	TIGO TGAT D TIGO TGAT 190 STCC S S 220	V V IGTT IGT IGT IGT IGT IGT IGT IGGGA	132 V 162 STAC Y 192 G G CGGZ	L 133 L 163 CTTC L 193 CGGC G G CTTC 223	Y Taken the second seco	135 CATC M 165 ATCC S 195 CGGC CS G 225	Tide D Tide CAGO S Tide SAGO S ZZC	P 167 167 CCAAC K 197 227 FTCC	MATC M 168 GGA7 198 GGA7 228 GAA7	139 GTGC C 169 CAT <i>I</i> 199 AGTT V 229	

Expression cassette of pYSG-IBA23, continued



LacP/Z cassette = contains LacZ alpha fragment under control of a separate promoter, which allows alpha complementation of *LacZ* mutations such as *LacZM15* as in *E. coli* DH5a or TOP10. after StarGate cloning using *Esp*3I your gene of interest will be located here

Features	from bp	to bp	Sequencing primer
LEU2d	1668	574	YSG-Primer-for (Cat. No. 5-0000-141)
2 micron ori	2032	3194	
URA3	4293	3490	5'- CAATATCATATAGAAGTCATCGA -3'
Ampicillin resistance gene	4725	5585	
ColElori	5756	6345	YSG-Primer-rev (Cat. No. 5-0000-142)
CUP1 promoter	6873	6925	13G-Fillier-lev (Cat. No. 5-0000-142)
forward primer binding site	6939	6961	5'- GCAGCTACCACATTGGCATTGGC -3'
GST-tag	7049	7702	
PreScission [™] Protease site (PCS)	7703	7750	
LacZ alpha fragment	7979	8380	\Box
Strep-tag	8444	8476	
reverse primer binding site	8517	8539	\Box
total vector length		8540	



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